



AFRL-SA-WP-SR-2016-0001

**DoD Global, Laboratory-
Based, Influenza Surveillance
Program, End-of-Year Report,
2014-2015**



Laurie DeMarcus



January 2016

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U.S. Air Force School of Aerospace Medicine
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14. ABSTRACT This is the cumulative report for specimens tested at USAFSAM during the 2014-2015 influenza season (28 September 2014 to 3 October 2015). During this period, results were finalized for 6,233 specimens from 89 locations. There were 2,058 specimens positive for influenza (four A(H1N1)pdm09, 1,792 A(H3N2), 34 B/Victoria, 83 B/Yamagata, 139 B/unknown lineage, and six influenza co-infections). Differences between specimens collected and tested are due to specimens sent for sequencing only and/or specimens not tested for various reasons. Of 6,233 influenza-like illness (ILI) cases, 2,403 are service members (38.6%), 2,395 are children (38.4%), 953 (15.3%) are spouses, and 482 (7.7%) are retirees and other beneficiaries. There are no unknown beneficiary types. The median age of ILI cases with known age (n=6,222) is 23.0 (range 0, 95) and 2,397 (38.5%) of these specimens are from ILI cases less than 18 years of age.					
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DoD Global, Laboratory-Based, Influenza Surveillance Program



USAF School of Aerospace Medicine

2014 - 2015

Cumulative Results

Season	
Locations	89
Collected	6,291
Tested	6,233
Influenza A	1,801
A(H1N1)pdm09	4
A(H3N2)	1,792
A & B	1
A & Parainfluenza	1
A(H3N2) & B/Victoria & Adenovirus & Rhino/Enterovirus	1
A(H3N2) & Coronavirus	1
A(H3N2) & Rhino/Enterovirus	1
Influenza B	257
B*	139
B & Rhino/Enterovirus	1
B/Victoria	34
B/Yamagata	83
Other Respiratory Pathogens	1,173
Adenovirus	128
<i>Bordetella pertussis</i>	0
<i>Chlamydomphila pneumoniae</i>	2
Coronavirus	91
Human	71
Metapneumovirus	
<i>Mycoplasma pneumoniae</i>	48
Parainfluenza	180
RSV	208
Rhino/Enterovirus	320
Non-influenza Co-infections	125

*USAFSAM does not sequence all influenza B specimens to determine lineage.

Lab data are current as of 26 October 2015.



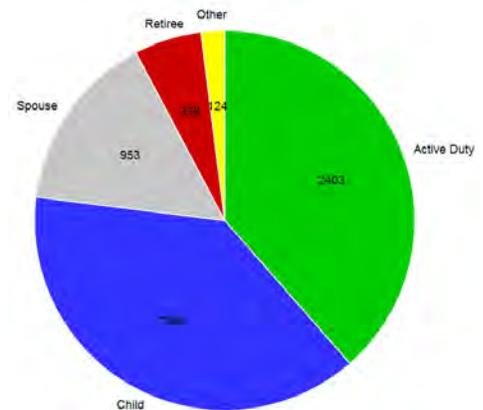
Respiratory Highlights 2014-2015 Influenza Season (28 September 2014 - 3 October 2015)

- During the 2014-2015 influenza season (28 September 2014 - 3 October 2015), results were finalized for 6,233 specimens from 89 locations. There were 2,058 specimens positive for influenza (four A(H1N1)pdm09, 1,792 A(H3N2), 34 B/Victoria, 83 B/Yamagata, 139 B/unknown lineage, and six influenza co-infections). See Table 2 on pages 5 & 6 for these results and other respiratory pathogens identified. Differences between specimens collected and tested are due to specimens sent for sequencing only and/or specimens not tested for various reasons.
- This is the cumulative report for specimens tested at USAFSAM during the 2014-2015 influenza season.

Table 1. ILI by age group for the 2014-2015 surveillance year

Age Group	Frequency	Percent
0-5	1346	21.59
6-9	463	7.43
10-17	588	9.43
18-24	920	14.76
25-44	2075	33.29
45-64	640	10.27
65+	190	3.05
Unknown	11	0.18

Graph 1. ILI by beneficiary status for the 2014-2015 surveillance year



Demographic Summary

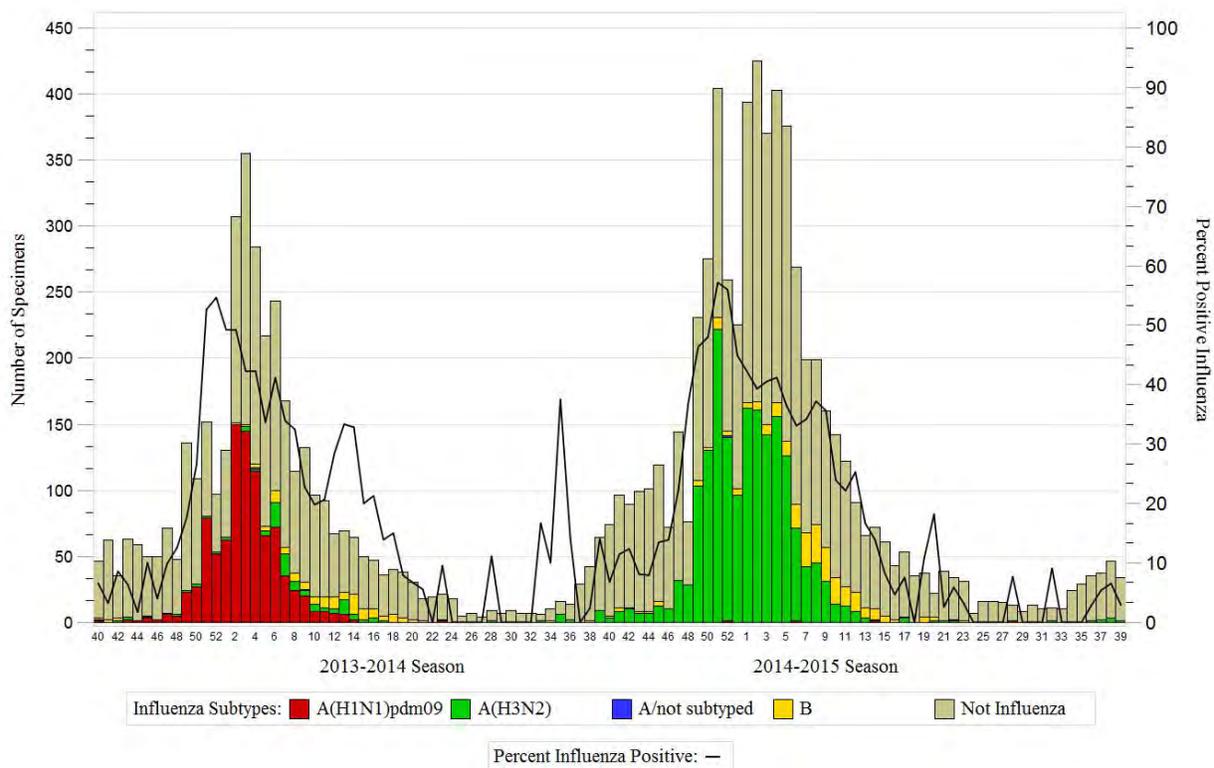
Of 6,233 ILI cases, 2,403 are service members (38.6%), 2,395 are children (38.4%), 953 (15.3%) are spouses, and 482 (7.7%) are retirees & other beneficiaries. There are no unknown beneficiary types. The median age of ILI cases with known age (n=6,222) is 23.0 (range 0, 95) and 2,397 (38.5%) of these specimens are from ILI cases less than 18 years of age.

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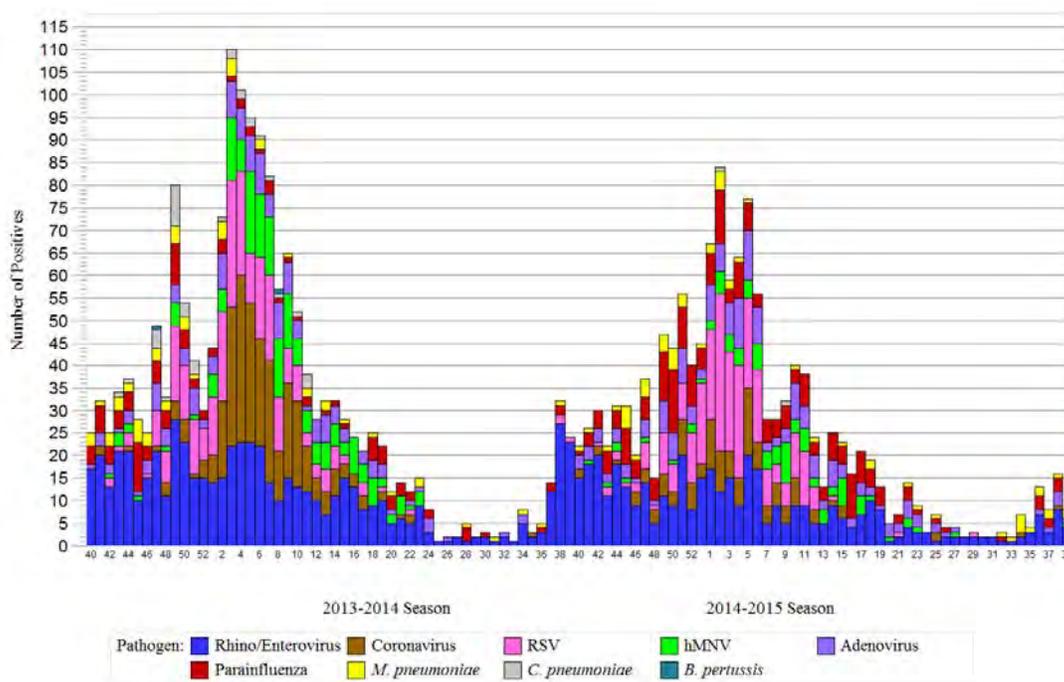
Laboratory Results - Cumulative for Season

Graph 2. Percent influenza positive by week for the 2013-2014 & 2014-2015 surveillance years



Note: One specimen positive for influenza A(H3N2)v has been excluded from the graph during the 2013-2014 season and two dual influenza co-infections have been excluded from the graph during the 2014-2015 season.

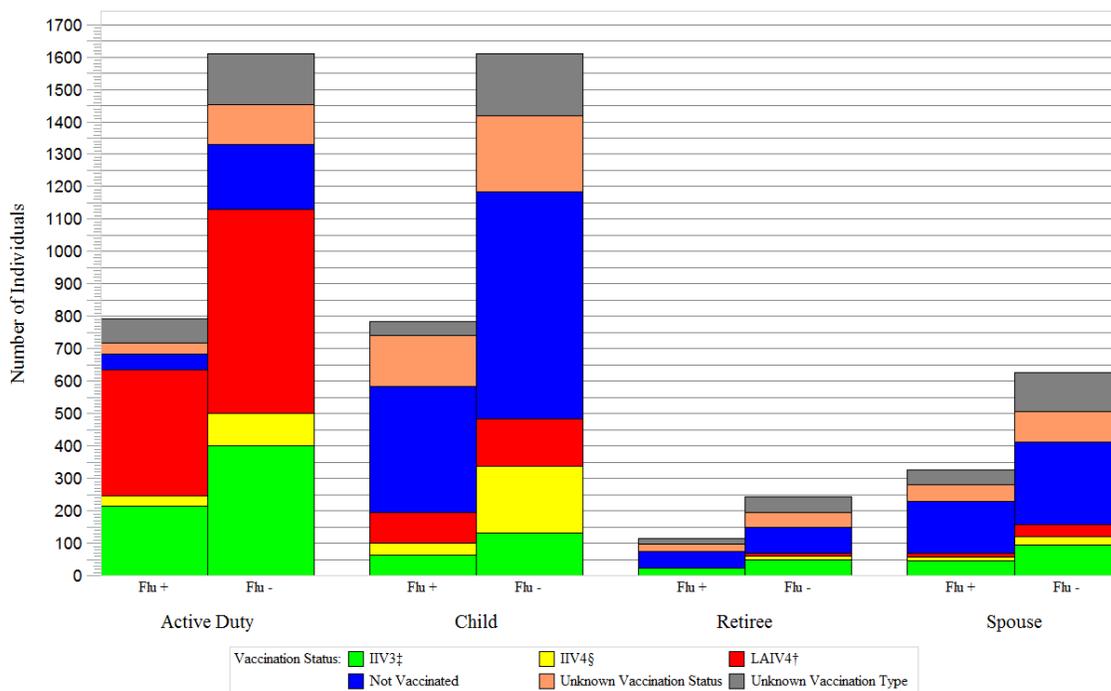
Graph 3. Other respiratory pathogen results by week for the 2013-2014 & 2014-2015 surveillance years



Note: Due to change in protocol between the surveillance years, 2013-2014 and 2014-2015, a direct comparison between the years cannot be made.

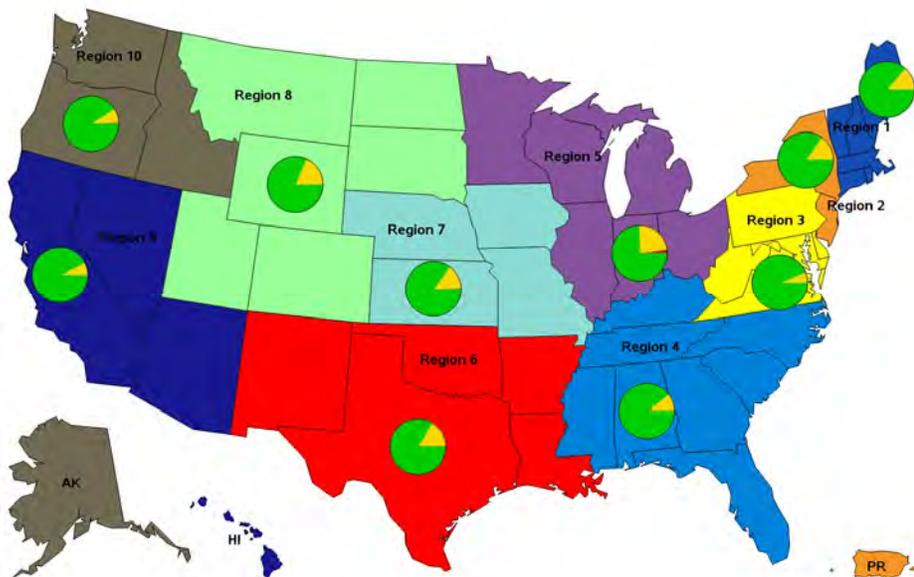
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Graph 4. Vaccination status by beneficiary type for the 2014-2015 surveillance year

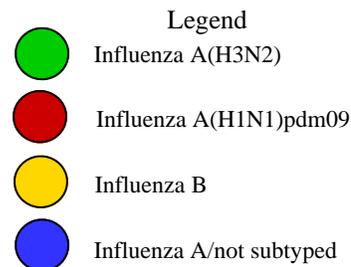


- ‡ Influenza Injectable Vaccine (trivalent)
- § Influenza Injectable Vaccine (quadrivalent)
- † Live Attenuated Influenza Vaccine (quadrivalent)

Map 1. Influenza subtypes by Health & Human Service regions for the 2014-2015 surveillance year



Region	Flu (+)	Flu (-)	% Positive
Region 1	58	85	40.56
Region 2	228	398	36.42
Region 3	46	68	40.35
Region 4	440	889	33.11
Region 5	47	110	29.94
Region 6	306	684	30.91
Region 7	133	243	35.37
Region 8	245	373	39.64
Region 9	163	439	27.08
Region 10	153	610	20.05



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Map 2. Influenza subtypes by country for the 2014-2015 surveillance year (Pacific)



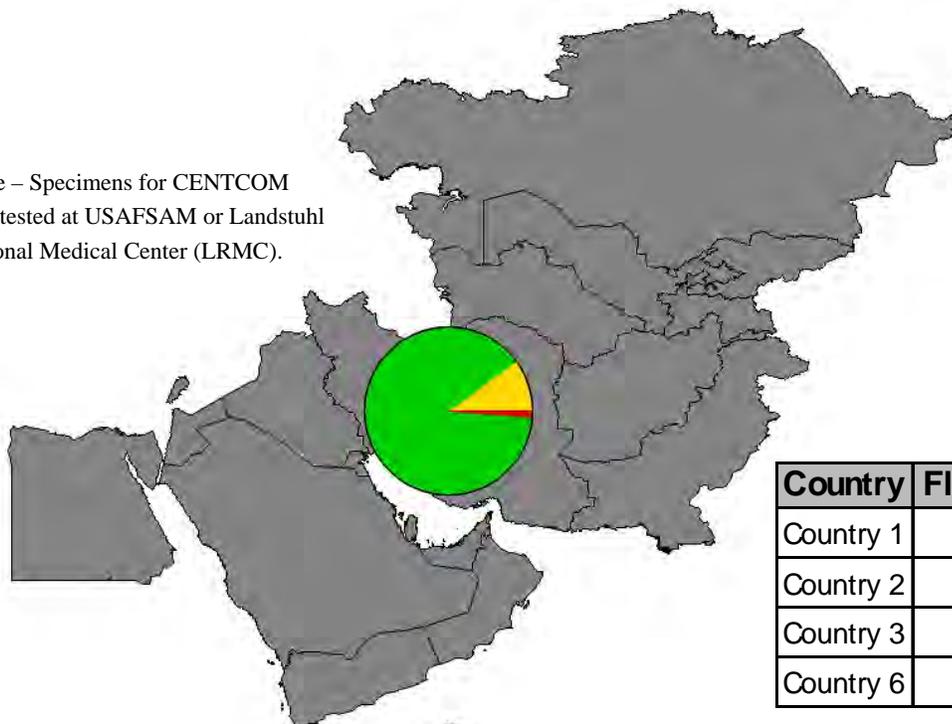
Country	Flu (+)	Flu (-)	% Positive
Guam	16	47	25.40
Japan	108	103	51.18
South Korea	26	10	72.22



- Legend
- Influenza A(H3N2)
 - Influenza A(H1N1)pdm09
 - Influenza B
 - Influenza A/not subtyped

Map 3. Influenza subtypes for CENTCOM for the 2014-2015 surveillance year

*Note – Specimens for CENTCOM were tested at USAFSAM or Landstuhl Regional Medical Center (LRMC).



Countries marked in blue contain sentinel sites (Pacific map only).

Country	Flu (+)	Flu (-)	% Positive
Country 1	27	80	25.23
Country 2	58	36	61.70
Country 3	2	0	100.00
Country 6	2	49	3.92

DoD Global, Laboratory-Based, Influenza Surveillance Program

Laboratory Results—2014-2015 surveillance year

Table 2. Cumulative results by region and location

Region*		A(H1N1)pdm09	A(H3N2)	A/not subtyped & Para	A(H3N2) & B/Victoria & Adeno & Rhino/Entero	A(H3N2) & Corona	A(H3N2) & Rhino/Entero	Influenza A & B	B	B/Victoria	B/Y amagata	B & Rhino/Entero	Adenovirus	C. pneumoniae	Coronavirus	hMPNV	M. pneumoniae	Parainfluenza	RSV	Rhinovirus/Enterovirus	Non-Influenza Co-Infection	No Pathogen	Total
Deployed	Country 1, Location B	-	26	-	-	-	-	-	-	-	1	-	-	-	4	3	-	-	-	18	3	52	107
	Country 2, Location A	1	48	-	-	-	1	-	1	-	7	-	-	-	-	-	-	-	-	6	1	29	94
	Country 3, Location A	-	2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2
PACOM	CFA Okinawa, Japan	-	4	-	-	-	-	-	-	-	-	-	2	-	-	-	-	-	-	2	-	20	28
	Camp Zama, Japan	-	6	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	6
	Eielson AFB, AK	-	6	-	-	-	-	1	-	-	-	-	3	-	-	-	-	-	-	2	-	9	21
	JB Elmendorf-Richardson, AK	-	7	-	-	-	-	-	-	1	-	-	-	1	-	-	-	-	-	-	-	5	14
	JR Marianas - Andersen AFB, Guam	-	11	-	-	-	-	1	-	4	-	6	-	-	3	-	1	3	5	1	27	62	
	JR Marianas - NH Guam, Guam	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1
	Kadena AB, Japan	-	5	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	1	11	19
	Kunsan AB, South Korea	-	11	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	12
	Misawa AB, Japan	-	10	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	2	-	14	27
	Osan AB, South Korea	-	15	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	8	24
	Tripler AM C, HI	-	16	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	16
	Yokota AB, Japan	-	81	-	-	-	-	-	-	2	-	2	-	2	-	4	-	1	1	5	1	32	131
	Region 1	Hanscom AFB, MA	-	24	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	3	1	-	30
NHCNE Newport, RI		-	16	-	-	-	-	1	2	3	-	2	-	-	-	-	-	1	2	1	2	23	53
USCG Academy, CT		-	10	-	-	-	-	1	-	-	1	-	-	-	1	1	-	1	2	1	14	31	
Region 2	CGAS Borinquen, PR	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1
	Ft Drum, NY	-	64	-	-	-	-	13	-	9	-	5	-	5	5	1	4	10	19	10	59	204	
	JB McGuire-Dix-Lakehurst, NJ	-	32	-	-	1	-	-	-	2	-	-	-	-	-	-	-	-	2	6	1	34	78
Region 3	USMA - West Point, NY	1	96	-	-	-	-	8	-	2	-	6	-	9	2	5	8	12	11	8	175	343	
	CG Base Portsmouth, VA	-	5	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	5	
	Dover AFB, DE	-	21	-	-	-	-	-	-	1	-	-	-	1	1	1	1	-	-	-	-	20	46
	JB Anacostia-Bolling, DC	-	4	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	5
	JB Andrews, MD	-	4	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	1	2	-	4	12
	JB Langley-Eustis, VA	-	7	-	-	-	-	-	-	-	-	-	2	-	-	-	-	2	-	-	1	13	25
	NCRM - Ft Belvoir CH, VA	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	1	-	4	1	4	11
	NCRM - Walter Reed NM M C, MD	-	2	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	1	-	4
Region 4	NM C Portsmouth, VA	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	5	6
	CGSM obile, AL	-	11	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	2	-	9	23
	Columbus AFB, MS	-	7	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	1	-	20	29
	Eglin AFB, FL	-	14	-	-	-	-	3	-	2	-	3	-	-	1	1	4	6	4	7	66	111	
	Ft Bragg, NC	-	30	-	-	-	-	-	-	-	-	2	-	3	2	-	2	7	3	2	36	87	
	Ft Campbell, KY	-	30	-	-	-	-	1	1	-	5	-	1	1	-	4	2	6	3	37	91		
	Hurlburt Field, FL	-	22	-	-	-	-	1	-	-	3	-	-	-	2	1	4	9	2	41	85		
	JB Charleston (AF), SC	-	13	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	14
	JB Charleston (Navy), SC	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	2	-	2	5	
	Keesler AFB, MS	-	6	-	-	-	-	-	1	1	-	7	-	1	-	6	1	2	6	2	80	113	
	MacDill AFB, FL	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	13	13
	Maxwell AFB, AL	-	31	-	-	-	-	10	-	5	-	2	-	2	1	1	2	1	6	-	80	141	
	Moodys AFB, GA	-	92	-	-	-	-	5	3	3	-	16	-	8	10	1	17	5	22	11	109	302	
	NH Beaufort, SC	-	1	-	-	-	-	1	-	-	-	-	-	-	-	-	1	-	1	2	1	18	24
	NH Camp Lejeune, NC	-	61	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	3	12	77
	NH Jacksonville, FL	-	1	-	-	-	-	-	-	-	-	1	-	-	1	-	-	-	-	4	1	-	8
	Patrick AFB, FL	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	3	4
	Robins AFB, GA	-	35	-	-	-	-	3	-	2	-	1	-	3	1	-	-	-	-	-	-	43	88
	Seymour Johnson AFB, NC	-	15	-	-	-	-	-	-	-	-	2	-	-	1	-	1	3	5	-	-	13	40
	Shaw AFB, SC	-	7	-	-	-	-	-	-	-	-	-	-	-	1	-	1	-	1	2	-	13	25
Tyndall AFB, FL	-	14	-	-	-	-	-	-	3	-	4	-	1	1	-	1	2	1	1	17	45		
USCG Base Elizabeth City, NC	-	4	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	4	

*CONUS locations are based on Health & Human Services regions. Other locations are defined by COCOM.

** Refer to Table 3 for more detailed information on non-influenza co-infections.

Continued on page 6

DoD Global, Laboratory-Based, Influenza Surveillance Program

Laboratory Results—2014-2015 surveillance year

Table 2. Cumulative results by region and location (continued from page 5)

Region*		A(H1N1)pdm09	A(H3N2)	A/not subtyped & Para	A(H3N2) & B/Victoria & Adeno & Rhino/Entero	A(H3N2) & Corona	A(H3N2) & Rhino/Entero	Influenza A & B	B	B/Victoria	B/Yamagata	B & Rhino/Entero	Adenovirus	C. pneumoniae	Coronavirus	hMPV	M. pneumoniae	Parainfluenza	RSV	Rhinovirus/Enterovirus	Non-Influenza Co-Infection	No Pathogen	Total
Region 5	Scott AFB, IL	-	23	-	-	-	-	-	6	1	4	-	2	-	1	1	-	3	2	2	-	39	84
	Wright-Patterson AFB, OH	1	12	-	-	-	-	-	-	-	-	-	-	-	4	1	-	-	4	9	-	42	73
Region 6	Altus AFB, OK	-	16	-	-	-	-	-	4	-	2	1	3	-	1	-	-	6	7	4	2	118	164
	Barksdale AFB, LA	-	10	-	-	-	-	-	1	-	-	-	-	-	-	-	-	1	-	-	1	11	24
	Cannon AFB, NM	-	4	-	-	-	-	-	1	-	-	-	-	-	1	-	-	1	1	3	-	16	27
	Ft Hood, TX	-	2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2
	Holloman AFB, NM	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	4	5
	Laughlin AFB, TX	-	9	-	-	-	-	-	-	-	-	-	3	-	1	-	2	2	3	7	3	17	47
	Little Rock AFB, AR	-	18	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	34	53
	SAMMC, TX	-	3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3
	Sheppard AFB, TX	-	69	-	-	-	-	-	4	3	1	-	3	-	6	3	3	6	5	6	7	121	237
	Tinker AFB, OK	-	123	-	1	-	-	-	26	6	1	-	2	1	5	7	3	13	22	16	8	191	425
	USCG New Orleans, LA	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
	Vance AFB, OK	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	2	3
Region 7	Ft Leavenworth, KS	-	5	-	-	-	-	-	-	-	-	2	-	1	1	-	-	1	1	-	13	24	
	McConnell AFB, KS	-	38	1	-	-	1	2	-	2	-	-	-	3	-	-	1	-	4	-	28	80	
	Offutt AFB, NE	-	70	-	-	-	-	9	-	6	-	3	-	5	-	2	8	1	12	1	156	273	
Region 8	Buckley AFB, CO	-	2	-	-	-	-	1	2	-	-	-	-	1	-	-	-	1	1	-	9	17	
	Ellsworth AFB, SD	-	30	-	-	-	-	12	2	4	-	2	-	5	1	4	7	1	5	2	47	122	
	FE Warren AFB, WY	-	35	-	-	-	-	8	4	-	-	3	-	-	-	-	15	3	3	2	40	113	
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	Malmstrom AFB, MT	-	4	-	-	-	-	-	-	-	-	-	-	-	-	-	2	1	1	-	2	10	
	Minot AFB, ND	-	19	-	-	-	-	1	-	-	-	2	-	3	1	3	5	11	4	3	30	82	
	Peterson AFB, CO	-	50	-	-	-	-	1	2	3	-	-	-	-	1	1	4	3	4	2	41	112	
	USAF Academy, CO	-	26	-	-	-	-	2	1	-	-	-	-	-	-	1	1	-	2	-	31	64	
Region 9	Beale AFB, CA	-	2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	
	Davis-Monthan AFB, AZ	-	26	-	-	-	-	-	-	2	-	2	-	2	4	-	3	1	2	1	48	91	
	Edwards AFB, CA	-	8	-	-	-	-	1	1	1	-	-	-	-	-	-	3	-	-	-	16	30	
	Los Angeles AFB, CA	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	
	Luke AFB, AZ	-	12	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	-	-	15	29
	Nellis AFB, NV	-	19	-	-	-	-	1	2	2	-	2	-	-	-	-	-	2	2	-	31	61	
	Travis AFB, CA	-	56	-	-	-	-	1	1	-	-	1	-	2	2	2	12	18	14	3	216	328	
	USCG Island Alameda, CA	-	5	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3	8
	Vandenberg AFB, CA	-	6	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	3	-	26	36
Region 10	CGS North Bend, OR	-	2	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	1	-	1	5	
	Fairchild AFB, WA	-	22	-	-	-	-	1	-	1	-	1	-	2	2	-	1	7	1	1	11	50	
	Mountain Home AFB, ID	-	10	-	-	-	-	-	-	-	-	-	-	-	-	-	3	1	-	-	9	23	
	NH Bremerton, WA	1	92	-	-	-	-	7	-	2	-	18	1	5	7	5	25	39	40	21	387	650	
Total	4	1792	1	1	1	1	1	139	34	83	1	128	2	91	71	48	180	208	320	125	3002	6233	

*CONUS locations are based on Health & Human Services regions. Other locations are defined by COCOM.

** Refer to Table 3 for more detailed information on non-influenza co-infections.

DoD Global, Laboratory-Based, Influenza Surveillance Program

Laboratory Results—2014-2015 surveillance year

Table 3. Cumulative non-influenza co-infection results by region and location

Region*		Adeno & Corona	Adeno & Corona & Rhino/Entero	Adeno & Corona & Para & Rhino/Entero	Adeno & hMN	Adeno & Para	Adeno & Para & RSV & Rhino/Entero	Adeno & RSV	Adeno & RSV & Rhino/Entero	Adeno & Rhino/Entero	Corona & hMN	Corona & Para	Corona & RSV	Corona & RSV & Rhino/Entero	Corona & Rhino/Entero	hMN & RSV	hMN & Rhino/Entero	M. pneumo & Para	M. pneumo & RSV & Rhino/Entero	M. pneumo & Rhino/Entero	Para & RSV	Para & RSV & Rhino/Entero	Para & Rhino/Entero	RSV & Rhino/Entero	Total	
Deployed	Country 1, Location B	-	-	-	-	-	-	-	-	-	-	-	1	-	1	-	-	-	-	-	-	-	-	1	3	
	Country 2, Location A	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	
PACOM	JR Marianas - Andersen AFB, Guam	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1	
	Kadena AB, Japan	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	1	
	Osan AB, South Korea	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	
	Yokota AB, Japan	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	1	
Region 1	NHCNE Newport, RI	-	-	-	-	-	-	-	1	-	-	1	-	-	-	-	-	-	-	1	-	-	-	-	2	
	USCG Academy, CT	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	1	
Region 2	Ft Drum, NY	-	-	-	-	-	-	-	6	1	-	-	-	-	-	-	-	-	-	-	1	-	-	-	3	10
	JB M cGuire-Dix-Lakehurst, NJ	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	
	USM A - West Point, NY	-	-	-	-	-	1	-	2	-	1	-	-	1	-	-	-	-	-	-	-	1	2	-	8	
Region 3	JB Langley-Eustis, VA	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	
	NCRM - Ft Belvoir CH, VA	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	1	
	NCRM - Walter Reed NM MC, MD	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	1	
Region 4	Eglin AFB, FL	1	1	-	-	-	-	-	2	-	-	-	-	-	-	-	-	-	-	-	-	-	2	1	7	
	Ft Bragg, NC	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	1	-	2	
	Ft Campbell, KY	-	1	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	1	-	-	-	3	
	Hurlburt Field, FL	-	-	-	-	1	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	
	Keesler AFB, M S	-	-	1	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	
	Moody AFB, GA	-	-	-	-	-	-	-	3	-	-	-	-	1	-	1	-	-	2	-	-	2	2	2	11	
	NH Beaufort, SC	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	
	NH Camp Lejeune, NC	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	2	3	
	NH Jacksonville, FL	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	1	1	
	Tyndall AFB, FL	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	1	
Region 6	Altus AFB, OK	-	-	-	-	-	-	-	2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2		
	Barksdale AFB, LA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1	
	Laughlin AFB, TX	-	-	-	-	-	-	-	1	-	1	-	-	-	-	-	-	-	-	-	-	-	1	-	3	
	Sheppard AFB, TX	-	-	-	-	-	-	-	-	-	-	-	1	2	-	1	-	-	-	-	-	-	1	2	7	
	Tinker AFB, OK	-	-	-	1	1	-	-	1	-	-	-	-	-	-	1	2	-	-	-	-	-	-	2	8	
Region 7	Offutt AFB, NE	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1	
Region 8	Ellsworth AFB, SD	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1	-	2	
	FE Warren AFB, WY	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	1	2	
	Hill AFB, UT	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	1	-	-	-	2	
	Minot AFB, ND	-	-	-	-	-	-	1	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	1	3	
	Peterson AFB, CO	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	1	2	
Region 9	Davis-Monthan AFB, AZ	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	
	Travis AFB, CA	-	-	-	-	-	-	-	-	-	-	2	-	-	-	-	-	-	-	-	-	-	1	-	3	
Region 10	Fairchild AFB, WA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	1	
	NH Bremerton, WA	-	-	-	-	-	-	3	1	1	2	-	1	-	4	-	1	2	1	-	2	3	2	3	21	
Total		1	3	1	1	2	1	2	1	26	2	3	10	1	9	1	9	1	1	9	3	2	14	22	125	

*CONUS locations are based on Health & Human Services regions. Other locations are defined by COCOM.

EUCOM Respiratory Surveillance Supplemental Report Through 2014-2015

- In cooperation and agreement with U.S. Army Public Health Command Region-Europe (PHCR-E), the DoD Global, Laboratory-based, Influenza Surveillance Program has analyzed data from surveillance sites that submit specimens to Landstuhl Regional Medical Center (LRMC), Germany. LRMC's laboratory is the forward laboratory for military sites in Europe.

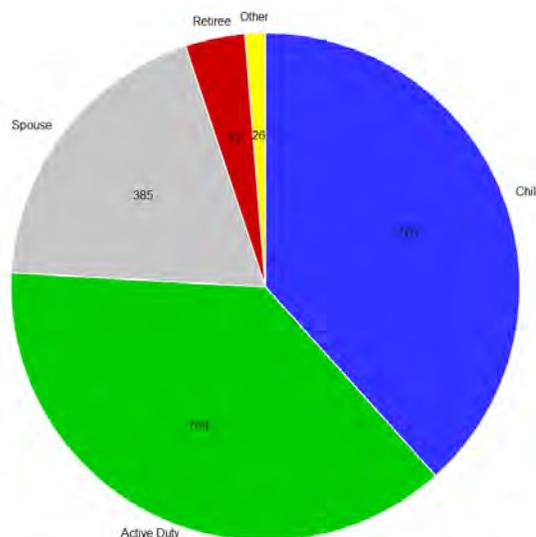
Table 4. Cumulative results by region and location for specimens collected during the 2014-2015 surveillance year

Region	A(H1N1)pdm09	A(H3N2)	A/not subtyped	A/not subtyped & RSV	A/not subtyped & Rhino/Entero	A(H1N1)pdm09 & hMNV	A(H1N1)pdm09 & RSV	A(H3N2) & B	A(H3N2) & hMNV	A(H3N2) & hMNV & Rhino/Entero	A(H3N2) & Para	A(H3N2) & RSV	A(H3N2) & RSV & Rhino/Entero	A(H3N2) & Rhino/Entero	Influenza A & B	B	B & RSV	B & Rhino/Entero	Adenovirus	hMNV	Parainfluenza	RSV	Rhinovirus/Enterovirus	Adeno & RSV	Adeno & RSV & Rhino/Entero	Adeno & Rhino/Entero	hMNV & RSV	hMNV & Rhino/Entero	Para & RSV	Para & Rhino/Entero	RSV & Rhino/Entero	No Pathogen	Total	
Deployed Country 6, Location A	-	2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	8	-	-	-	-	-	-	-	-	-	40	50
EUCOM Aviano AB, Italy	4	12	2	-	-	-	-	2	-	-	-	-	-	-	-	3	-	-	-	-	-	-	2	-	-	-	-	-	-	-	-	-	19	44
Incirlik AB, Turkey	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	1	2	6	2	6	-	-	1	-	-	-	-	-	-	17	37
Landstuhl RM C, Germany	5	108	11	-	1	1	-	-	-	-	-	2	-	-	2	10	-	-	1	7	10	46	46	2	1	6	2	-	1	2	7	195	466	
NAS Sigonella, Italy	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	1	2
NAVSTA Rota, Spain	3	15	-	1	-	-	-	-	-	-	-	-	-	-	-	4	-	1	1	2	-	2	5	-	-	1	-	-	-	-	-	1	34	70
NSA Naples, Italy	10	10	1	-	-	-	1	-	-	-	-	-	-	-	3	-	1	-	1	1	8	11	-	-	-	-	-	-	-	-	2	28	77	
RAF Lakenheath, England	5	132	3	-	3	-	-	-	-	1	3	-	9	-	11	1	-	2	8	9	12	58	-	-	1	-	1	1	3	9	167	439		
Ramstein AB, Germany	1	59	1	-	1	-	-	-	-	-	-	-	2	-	2	-	1	-	4	2	17	18	-	-	1	-	-	-	2	1	29	141		
Spangdahlem AB, Germany	1	21	1	1	-	-	-	1	-	1	-	2	-	1	-	-	1	4	5	13	6	-	-	1	-	-	-	-	-	3	35	97		
USAG Stuttgart, Germany	1	61	7	-	-	-	1	-	-	-	1	-	2	-	8	-	-	1	4	7	8	24	-	-	-	-	-	-	-	-	1	80	206	
USAG Vicenza, Italy	6	51	2	-	-	-	1	-	-	-	-	4	-	-	-	-	1	-	3	2	-	24	-	-	-	-	-	-	-	-	-	59	153	
Vilseck AHC, Germany	1	95	4	-	1	-	2	-	-	-	4	2	3	-	6	-	2	3	1	4	21	35	-	-	2	-	2	-	-	4	50	242		
Total	37	566	32	2	6	1	3	3	1	1	12	2	23	2	48	1	6	10	36	46	129	244	2	1	13	2	3	2	7	28	754	2024		

Table 5. ILI by age group for the 2014-2015 surveillance year

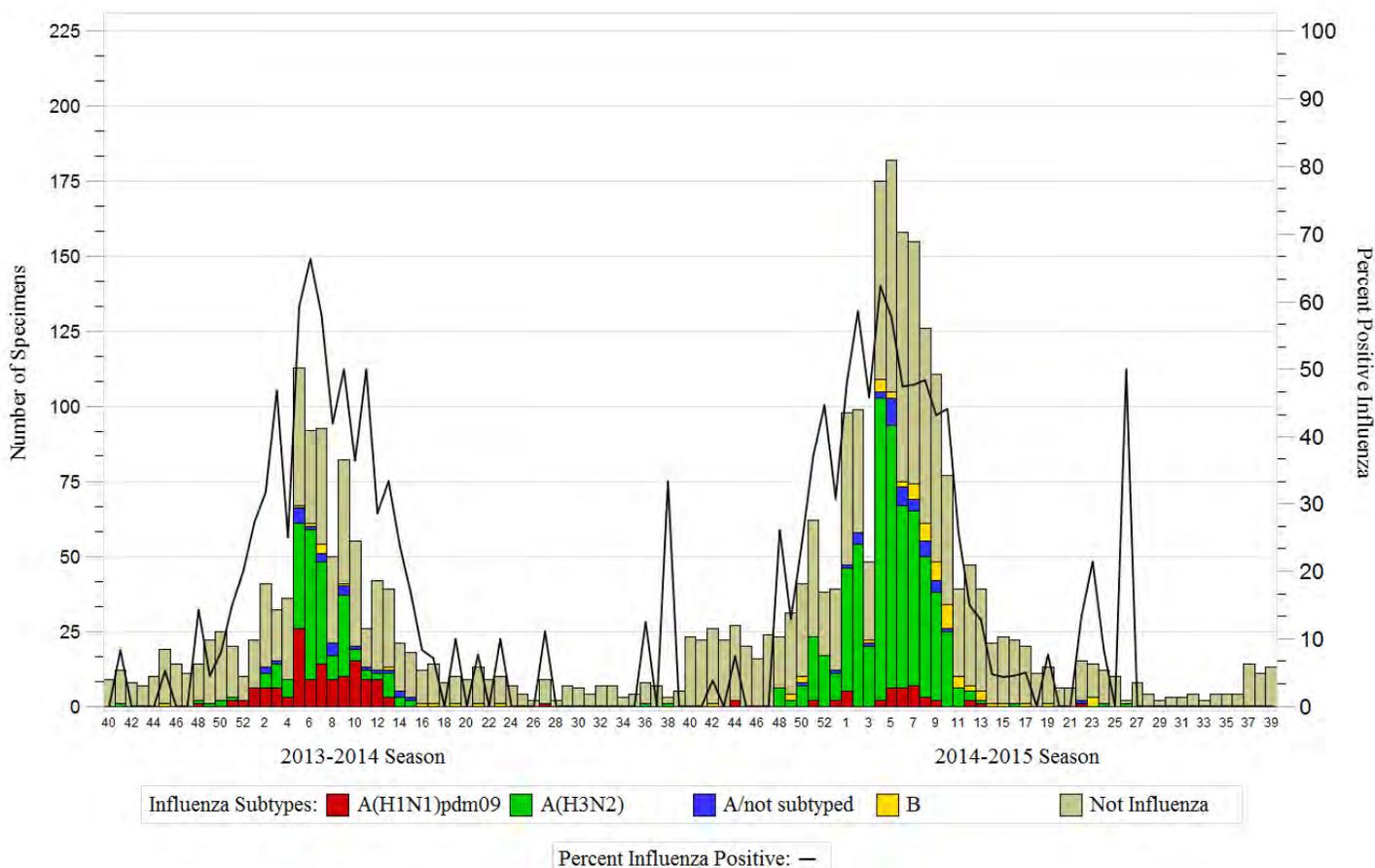
Age Group	Frequency	Percent
0-5	529	26.14
6-9	124	6.13
10-17	123	6.08
18-24	257	12.7
25-44	782	38.64
45-64	172	8.5
65+	37	1.83

Graph 5. ILI by beneficiary status for the 2014-2015 surveillance year



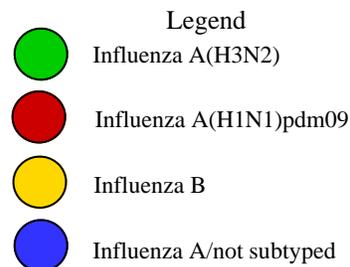
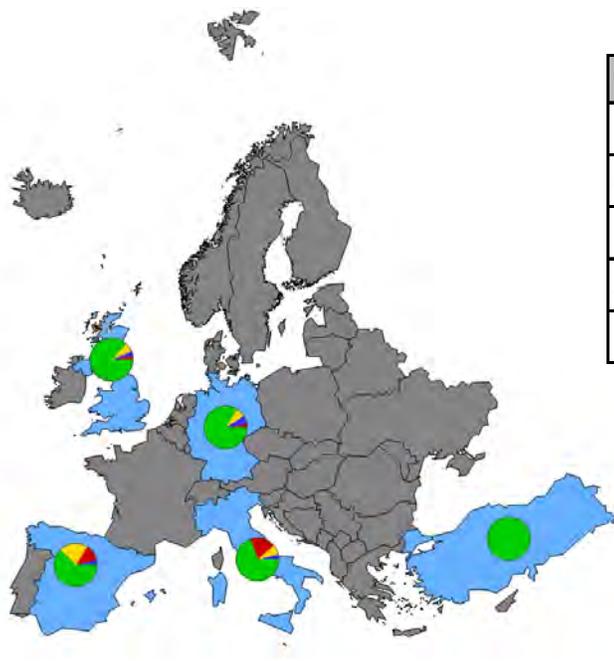
DoD Global, Laboratory-Based, Influenza Surveillance Program

Graph 6. Percent influenza positive by week for the 2013-2014 & 2014-2015 surveillance years (Europe)



Map 4. Percentage of influenza positive by country for the 2014-2015 surveillance year (Europe)

Country	Flu (+)	Flu (-)	% Positive
England	168	271	38.27
Germany	434	715	37.77
Italy	112	162	40.88
Spain	24	46	34.29
Turkey	2	35	5.41



Countries marked in blue contain sentinel sites

DoD Global, Laboratory-Based, Influenza Surveillance Program

USAF School of Aerospace Medicine

2014 - 2015

Respiratory Surveillance
2014-2015 Year
(beginning 28 September 2014)



USAF School of Aerospace Medicine

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Contributions to the CDC for National Influenza Surveillance

All sequence data are sent to the CDC and selected original specimens or isolates are sent for further characterization and possible use as influenza vaccine seed viruses. Specimens may also undergo antiviral testing.

DoD Global Influenza Surveillance Program

<https://gumbo2.wpafb.af.mil/epi-consult/index.cfm>

Background

The DoD-wide program was established by the Global Emerging Infections Surveillance and Response System (GEIS) in 1997. The surveillance network includes the US Air Force School of Aerospace Medicine (USAFSAM) (sentinel site respiratory surveillance), the Naval Health Research Center (recruit and shipboard population-based respiratory surveillance), the Naval Medical Research Unit (NAMRU-3) in Cairo, Egypt, the Naval Medical Research Unit (NAMRU-2) in Phnom Penh, Cambodia, the Armed Forces Research Institute of Medical Sciences (AFRIMS) in Bangkok, Thailand, the Naval Medical Research Unit-6 (NAMRU-6) in Lima, Peru, and the United States Army Medical Research Unit-Kenya (USAMRU-K) located in Nairobi, Kenya. This work is supported by the Air Force and the Division of Global Emerging Infections Surveillance and Response System (GEIS) Operations, a Division of the Armed Forces Health Surveillance Center (AFHSC).

Sentinel Site Surveillance at USAFSAM

In 1976, the US Air Force Medical Service began conducting routine, global, laboratory-based influenza surveillance. Air Force efforts expanded to DoD-wide in 1997. USAFSAM manages the surveillance program that includes global surveillance among DoD beneficiaries at over 90 sentinel sites (including deployed locations) and many non-sentinel sites (please see map on the left). Unique sentinel sites include three DoD overseas medical research laboratories (AFRIMS, NAMRU-6, USAMRU-K) and the US Army Public Health Command Region South (PHCR-S). These sites collect specimens from local residents in surrounding countries that may not otherwise be covered in existing surveillance efforts.

Since the 2006-2007 season, Landstuhl Regional Medical Center (LRMC) has served EUCOM as a USAFSAM contributing laboratory. The initiative seeks to provide more timely results and efficient transport of specimens.

For an expanded view of this report, visit our website. Also available on the website is a list of previous weekly surveillance reports, program information (including an educational briefing and instruction pamphlets for clinic staff), and an overview of historical data. Please visit the AFHSC/GEIS website for an overview of influenza surveillance at all collaborating organizations.

Errata:

Collaborating Partners

In addition to all participating DoD military sentinel sites, several collaborating partners (described above) may be further understood by reviewing the partner's website.



DoD Global, Laboratory-Based, Influenza Surveillance Program

Attachment - Molecular Sequence Analysis: 2014-2015 Season

USAFSAM Epidemiology Laboratory Service

This is a cumulative report for samples received at USAFSAM during the 2014-2015 season. Of the 1,006 total specimens and sequences collected and analyzed by USAFSAM between 4 September 2014 and 5 June 2015, 862 (86%) were influenza A(H3N2) viruses, 10 (1%) were influenza A(H1N1)pdm09 viruses, 94 (9%) were influenza B/Yamagata viruses, and 40 (4%) were influenza B/Victoria virus specimens.

CONUS	A(H3N2)	A(H1N1)pdm09	B/Yamagata	B/Victoria
Alabama, CGS Mobile	6		1	
Alabama, Maxwell AFB	13		5	
Arizona, Davis-Monthan AFB	8		2	
Arizona, Luke AFB	2			
Arkansas, Little Rock AFB	4			
California, Beale AFB	1			
California, Edwards AFB	5		1	1
California, NHRC	9			1
California, Travis AFB	19			1
California, USCG Island Alameda	1			
California, Vandenberg AFB	2			
Colorado, Buckley AFB	1			2
Colorado, Peterson AFB	20		3	2
Colorado, USAF Academy	13			1
Connecticut, USCG Academy	4			
Delaware, Dover AFB	11		1	
District of Columbia, JB Anacostia-Bolling	2			
Florida, Eglin AFB	7		2	
Florida, Hurlburt Field	8			
Florida, NH Jacksonville	1			
Florida, Tyndall AFB	8		3	
Georgia, Moody AFB	53		3	3
Georgia, Robins AFB	25		2	
Idaho, Mt Home AFB	4			
Illinois, NHRC	4			
Illinois, Scott AFB	7		4	1
Kansas, Ft Leavenworth	1			
Kansas, McConnell AFB	10		2	
Kentucky, Ft Campbell	13			1
Louisiana, Barksdale AFB	5			1
Louisiana, USCG New Orleans	1			
Maryland, JB Andrews	4			
Maryland, NCRM - Walter Reed NMMC	2			
Massachusetts, Hanscom AFB	9		1	
Mississippi, Columbus AFB	3			
Mississippi, Keesler AFB	4		1	1
Montana, Malmstrom AFB	1			
Nebraska, Offutt AFB	31		6	
Nevada, Nellis AFB	10		2	2
New Jersey, JB McGuire-Dix-Lakehurst	10		2	
New Mexico, Cannon AFB	1			
New Mexico, Holloman AFB	1			
New York, Ft Drum	19		9	
New York, USMA - West Point	26	1	2	
North Carolina, Ft Bragg	17			
North Carolina, NH Camp Lejeune	45			
North Carolina, Seymour Johnson AFB	8			
North Carolina, USCG Base Elizabeth City	1			
North Dakota, Minot AFB	6			
Ohio, Wright-Patterson AFB	1			
Oklahoma, Altus AFB	2		2	
Oklahoma, Tinker AFB	44		1	7
Oregon, CGS North Bend	1			
Rhode Island, NHCNE Newport	7		3	2
South Carolina, JB Charleston (AF)	5			
South Carolina, NH Beaufort	1			
South Carolina, Shaw AFB	4			
South Dakota, Ellsworth AFB	12		4	2
Texas, Ft Hood	1			
Texas, Laughlin AFB	2			
Texas, SAMMC	1		1	1
Texas, Sheppard AFB	33		1	3
Utah, Hill AFB	15		2	
Virginia, CG Base Portsmouth	3			
Virginia, JB Langley-Eustis	5			
Virginia, NMC Portsmouth	1			1
Washington, Fairchild AFB	6		1	
Washington, NH Bremerton	44		2	
Wyoming, FE Warren AFB	8			4
CONUS Total	662	1	69	37

OCONUS	A(H3N2)	A(H1N1)pdm09	B/Yamagata	B/Victoria
Belgium, Shape AHC	2			
Alaska, Eielson AFB	4			
Alaska, JB Elmendorf-Richardson	6		1	
Country 1, Location B	22		1	
Country 2, Location A	19	1	7	
Country 3, Location A	1			
England, RAF Lakenheath	1		1	
Germany, Kaiserslautern AHC	1			
Germany, Landstuhl RMC (ALL)	42	1	3	
Germany, Patch AHC	2		1	
Germany, Ramstein AB	1			
Germany, Spangdahlem AB	1			
Guam, JR Marianas-Andersen AFB	6		4	
Hawaii, Tripler AMC	10		1	
Indonesia, AFRIMS	3	1	1	
Italy, Aviano AB			1	
Italy, USAG Vicenza	6	5	1	
Japan, Camp Zama	4			
Japan, CFA Okinawa	3			
Japan, Kadena AB	4			
Japan, Misawa AB	5			
Japan, Yokota AB	38		2	
Pakistan, AFRIMS			1	
Singapore, NHRC	2			
South Korea, Kunsan AB	4			
South Korea, Osan AB	9			
Thailand, AFRIMS	4	1		3
OCONUS Total	200	9	25	3

	A(H3N2)	A(H1N1)pdm09	B/Yamagata	B/Victoria
CONUS & OCONUS TOTAL	862	10	94	40

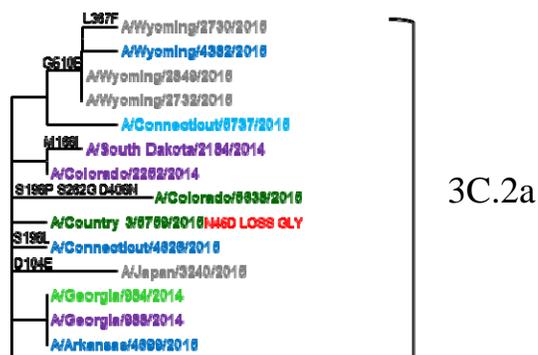
The hemagglutinin (HA) gene from select influenza positives was sequenced using dye terminator, Sanger-based methods. Preliminary data are based on the sequence analysis of the hemagglutinin gene. Antigenic sites, receptor binding sites and glycosylation motifs are predicated upon correlations with previously published experimental evidence.^{1,3,4} Sequence data was constructed and analyzed using multiple software programs. Genetic and predicted antigenic information that resulted from this analysis is shared with United States Centers for Disease Control and Prevention (CDC), World Health Organization (WHO) and potentially contributes to the seasonal Northern and Southern Hemisphere vaccine component selections.

Influenza A(H3N2)

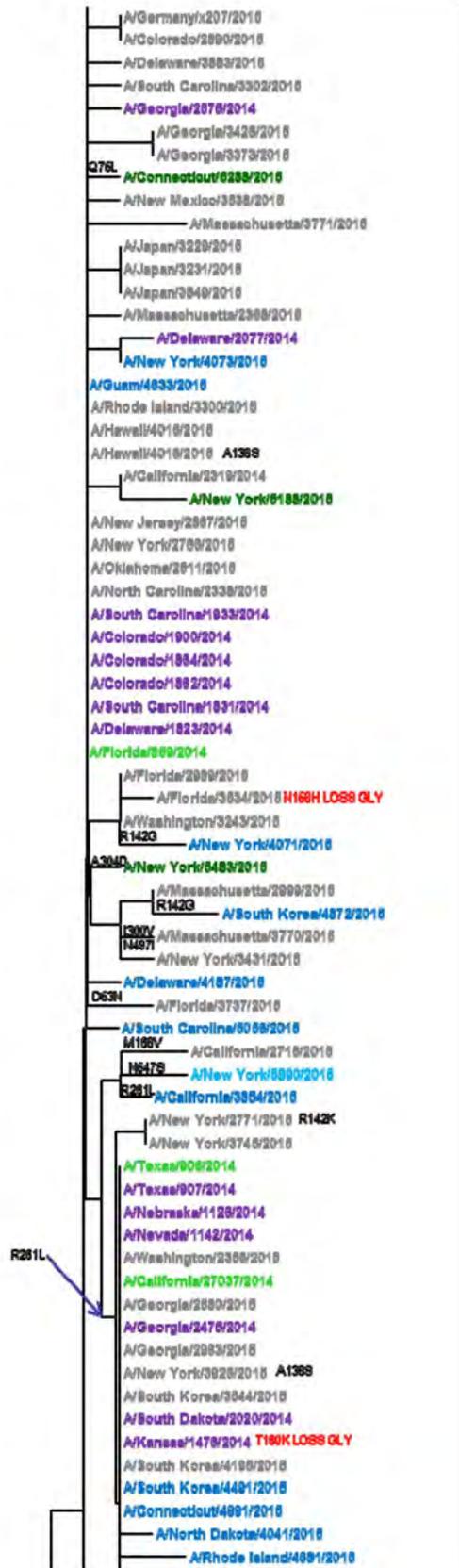
- Isolates are characterized in a neighbor-joining phylogenetic tree with reference strains rooted from the previous vaccine, A/Victoria/361/2011 [Figure 1].
- The influenza A(H3N2) specimens characterized for this report exhibited an overall protein identity of 96.9-99.1% as compared to the influenza A(H3N2) component of the 2013-2014 vaccine formulation, A/Texas/50/2012-like virus.
- Based on the mutations observed in reference to the root strain, A/Victoria/361/2011, all of the influenza A(H3N2) viruses analyzed belong to clade 3C, with 79% further classifying as 3C.2a and 21% further classifying as 3C.3 (6% 3C.3a).
- Gain or loss of *N*-linked glycosylation sites has been shown to alter HA protein surface topology. A gain in glycosylation could be advantageous to the virus by virtue of a masking effect on important antibody recognition sites, thus potentially modulating viral antigenicity.⁴ Observations are based solely on sequence motifs. For the influenza A(H3N2) specimens characterized in this report, 26 mutations were observed that could cause a loss of a glycosylation motif: N8D (asparagine to aspartic acid), T10A (threonine to alanine), T24M (threonine to methionine), N45D (asparagine to aspartic acid), N122D (asparagine to aspartic acid), S124G (serine to glycine), S124N (serine to asparagine), T128A (threonine to alanine), N133D (asparagine to aspartic acid), T135K (threonine to lysine), N144S (asparagine to serine), N158D (asparagine to aspartic acid), N158H (asparagine to histidine), N158K (asparagine to lysine), N158S (asparagine to serine), T160K (threonine to lysine), T160I (threonine to isoleucine), T160R (threonine to arginine), T160A (threonine to alanine), N246Y (asparagine to tyrosine), N246S (asparagine to serine), N246H (asparagine to histidine), T248A (threonine to alanine), T248I (threonine to isoleucine), T248K (threonine to lysine), and T485I (threonine to isoleucine). Three mutations, S144N (serine to asparagine), K160T (lysine to threonine), and I300T (isoleucine to threonine), were observed that could cause a gain of a glycosylation motif.
- Of the 163 mutations present in the influenza A(H3N2) specimens, 38 occurred at predicted antigenic sites and seven at the receptor binding site.^{2,5}

**USAFSAM 2014-2015 Season Cumulative Influenza A(H3N2)
HA Phylogenetic Analysis
Figure 1**

2014-2015 A(H3N2) Vaccine strain:
A/Texas/50/2012
2015-2016 A(H3N2) Vaccine strain:
A/Switzerland/9715293/2013
Reference Strain
September 2014
October 2014
November 2014
December 2014
January 2015
February 2015
March 2015
April 2015
May 2015
ADD GLY Create Glycosylation Motif
LOSS GLY Loss of Glycosylation Motif
F CDC Reference Antigen
e Egg Isolate
LR Low Reactor to : **A/Texas/50/2012** (≥8 fold)

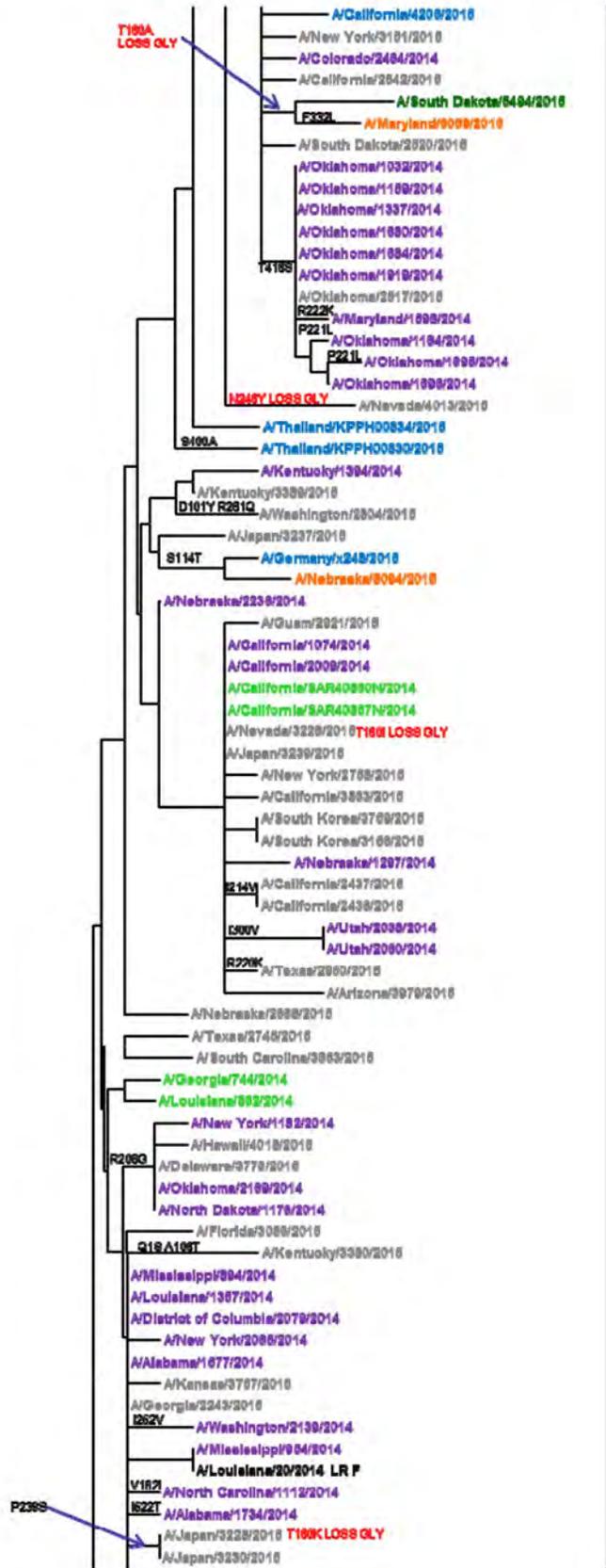


DoD Global, Laboratory-Based, Influenza Surveillance Program



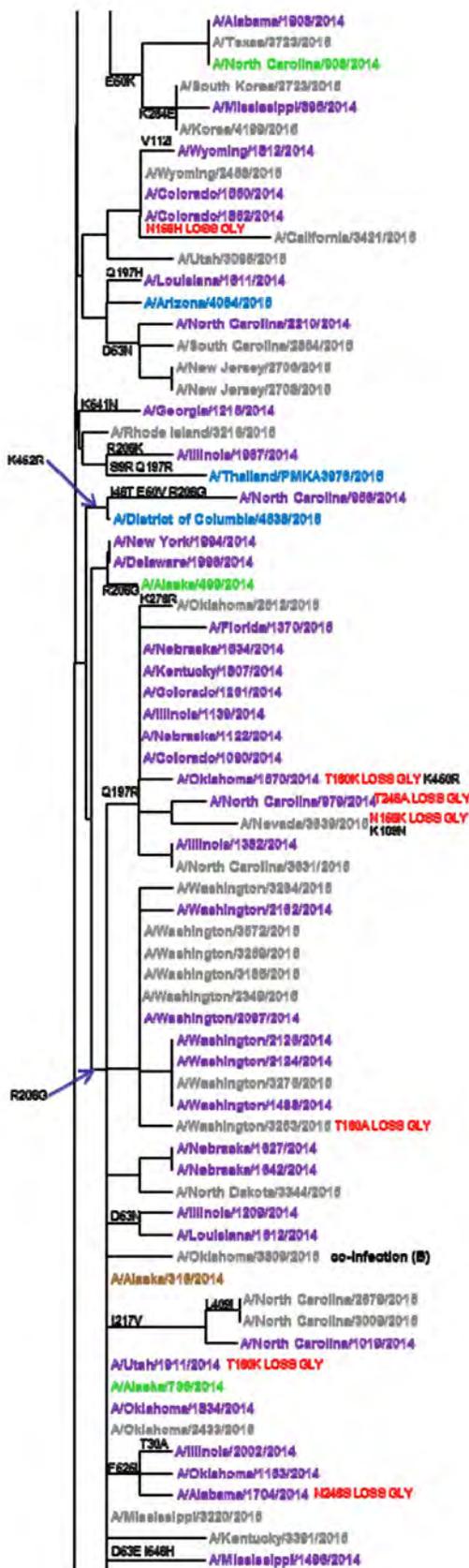
3C.2a

DoD Global, Laboratory-Based, Influenza Surveillance Program



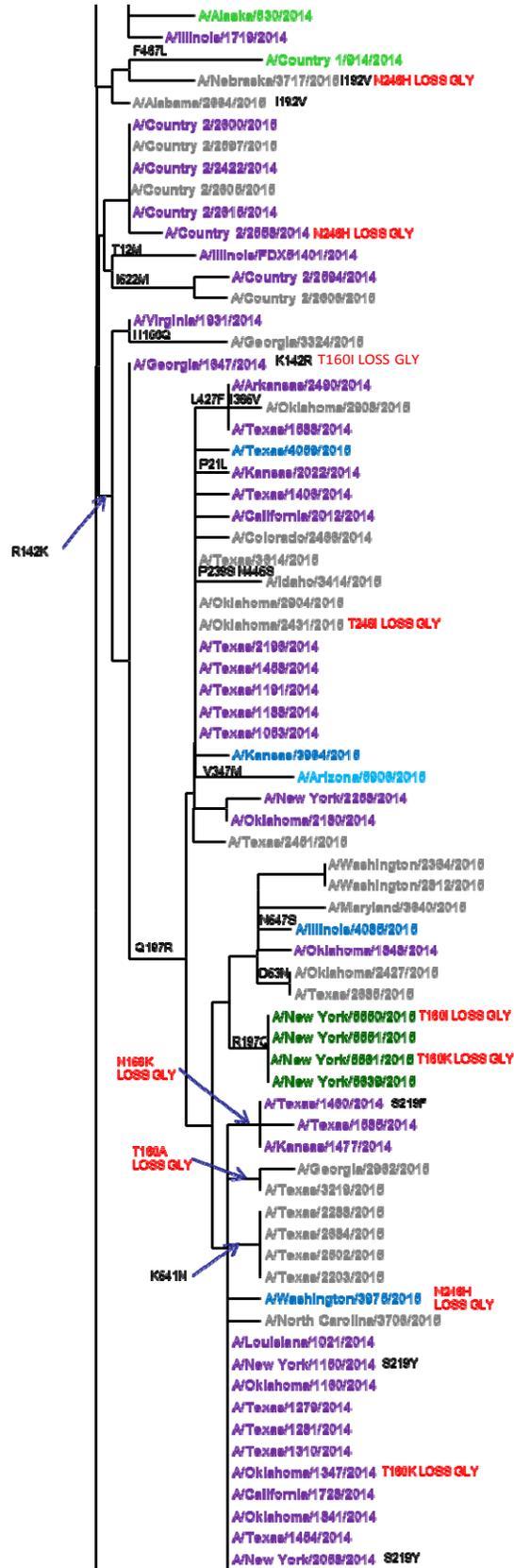
3C.2a

DoD Global, Laboratory-Based, Influenza Surveillance Program



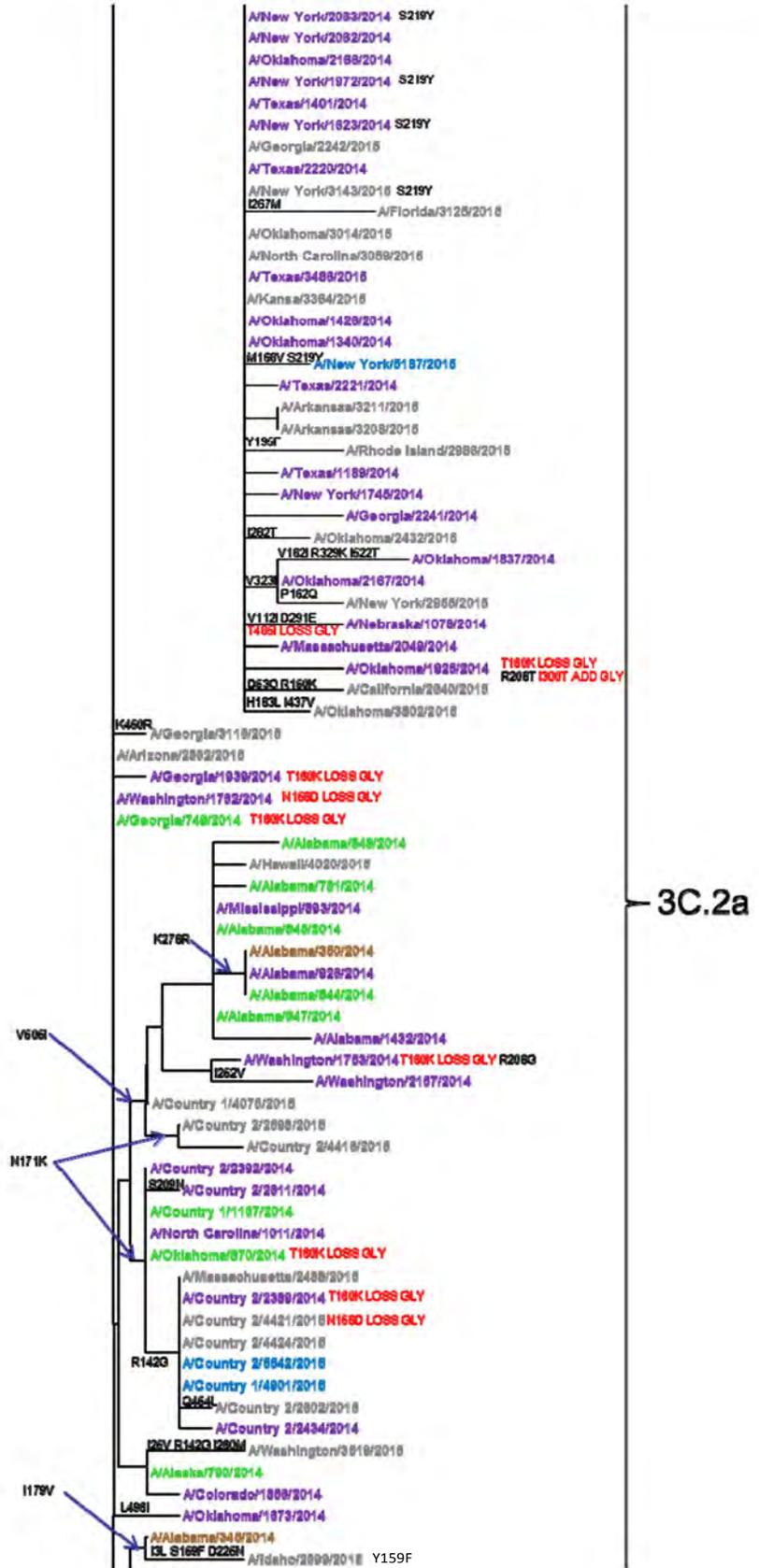
3C.2a

DoD Global, Laboratory-Based, Influenza Surveillance Program

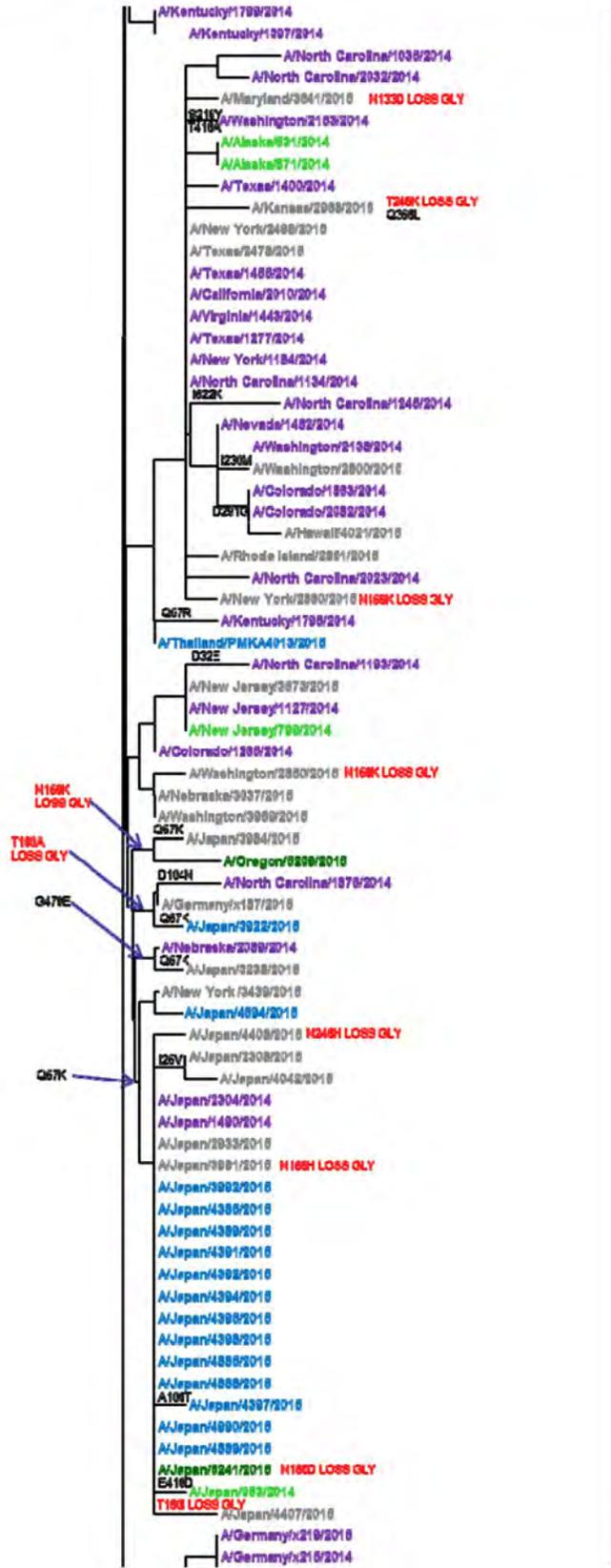


3C.2a

DoD Global, Laboratory-Based, Influenza Surveillance Program

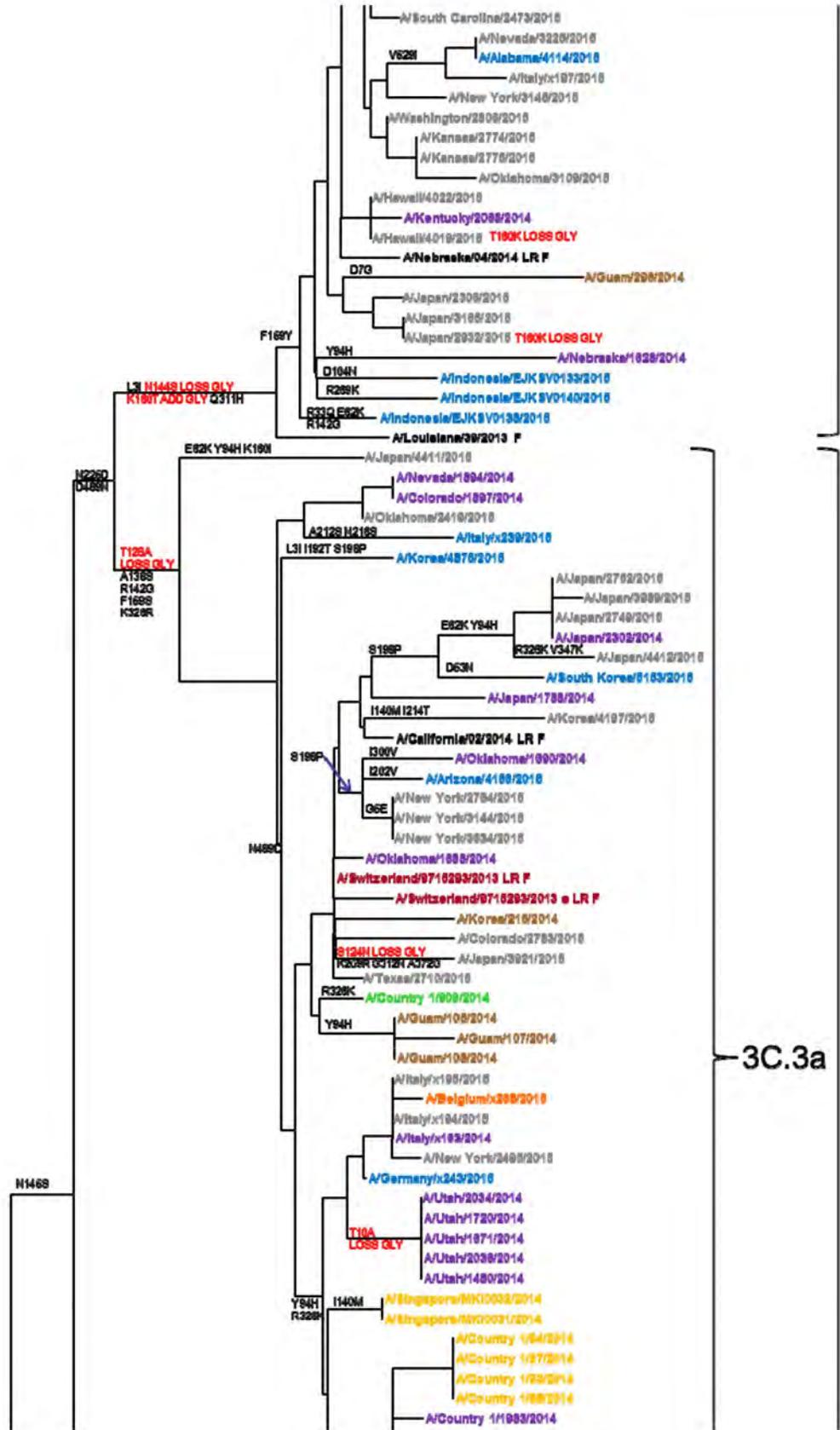


DoD Global, Laboratory-Based, Influenza Surveillance Program



3C.2a

DoD Global, Laboratory-Based, Influenza Surveillance Program

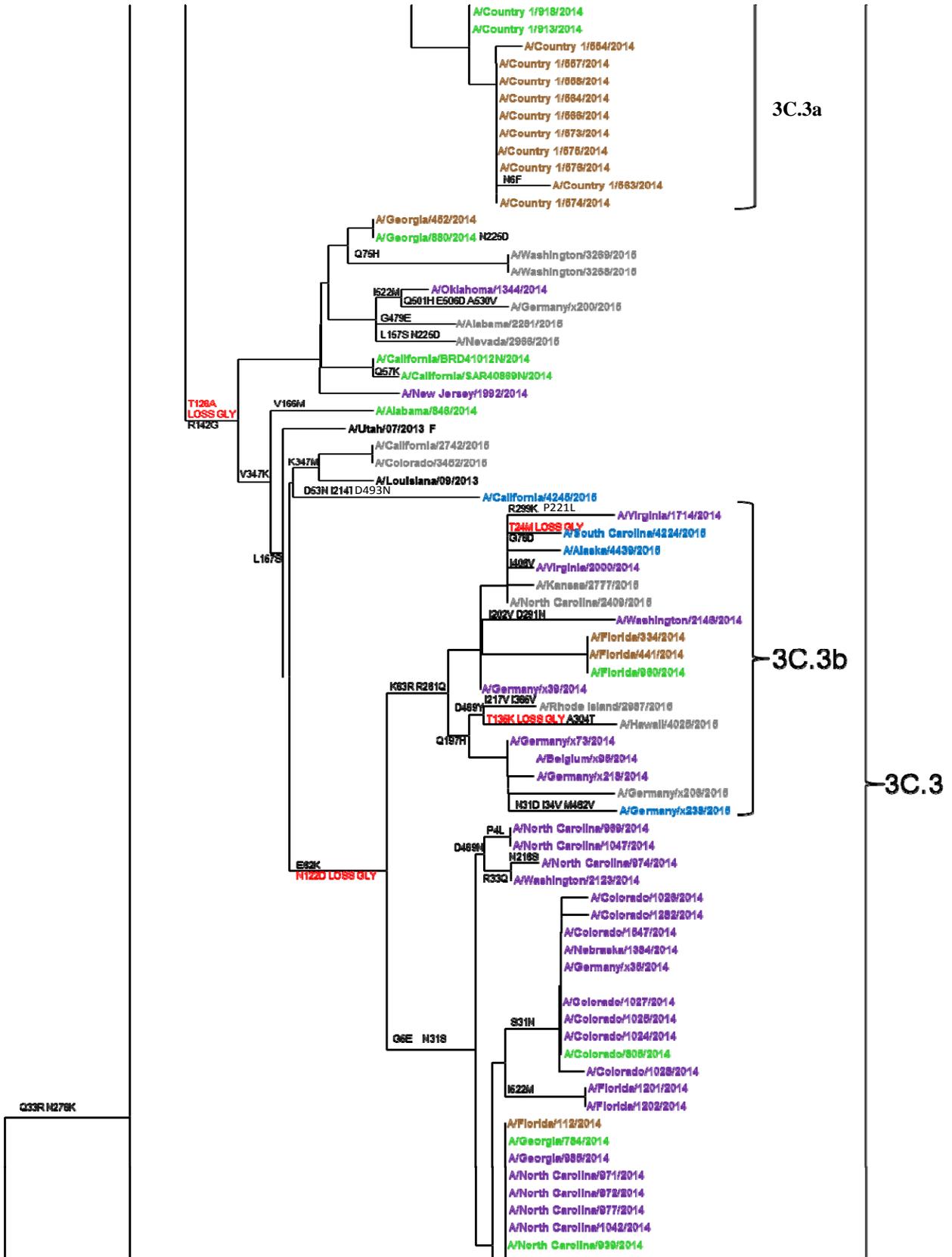


3C.2a

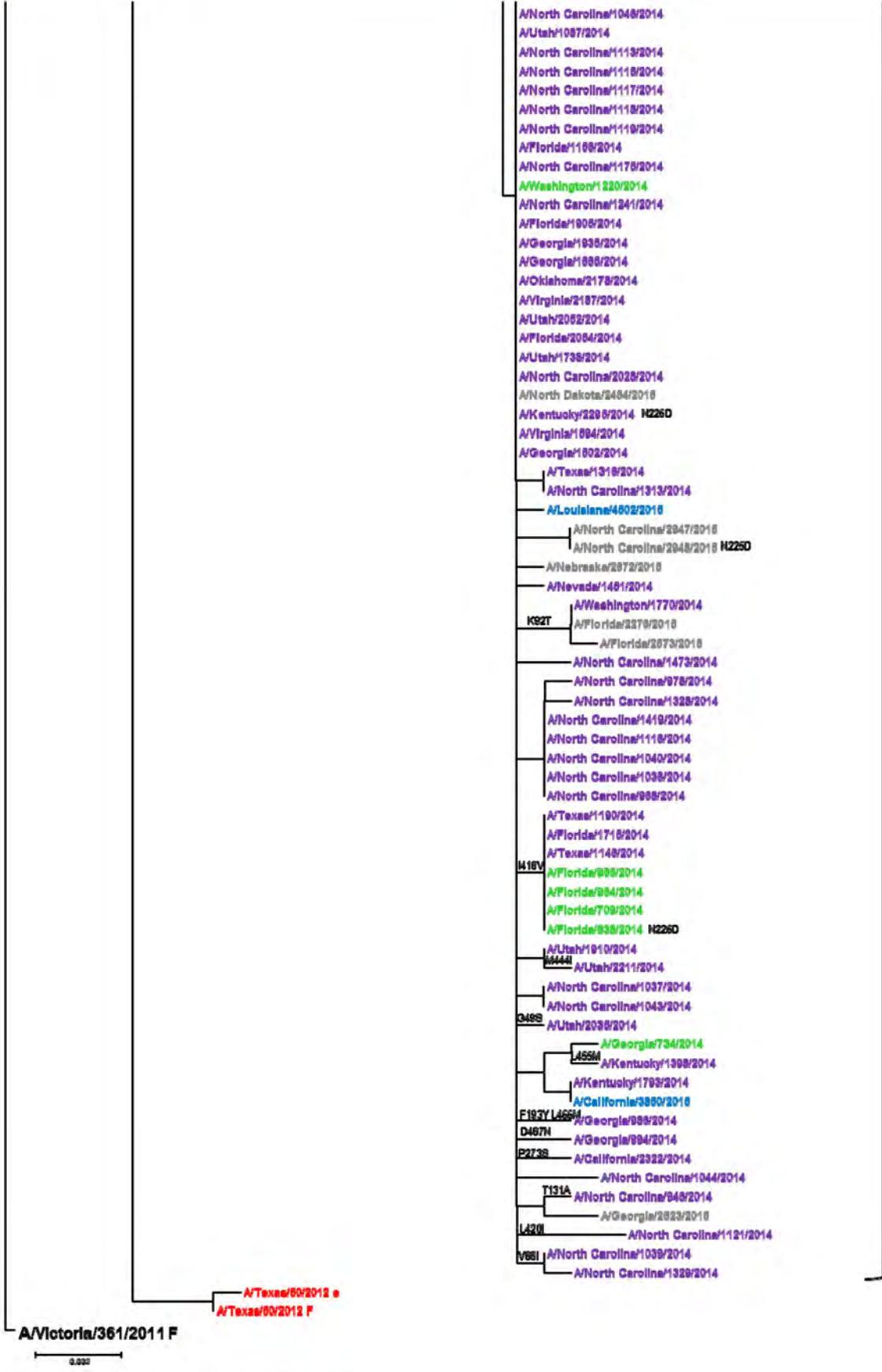
3C.3

3C.3a

DoD Global, Laboratory-Based, Influenza Surveillance Program



DoD Global, Laboratory-Based, Influenza Surveillance Program

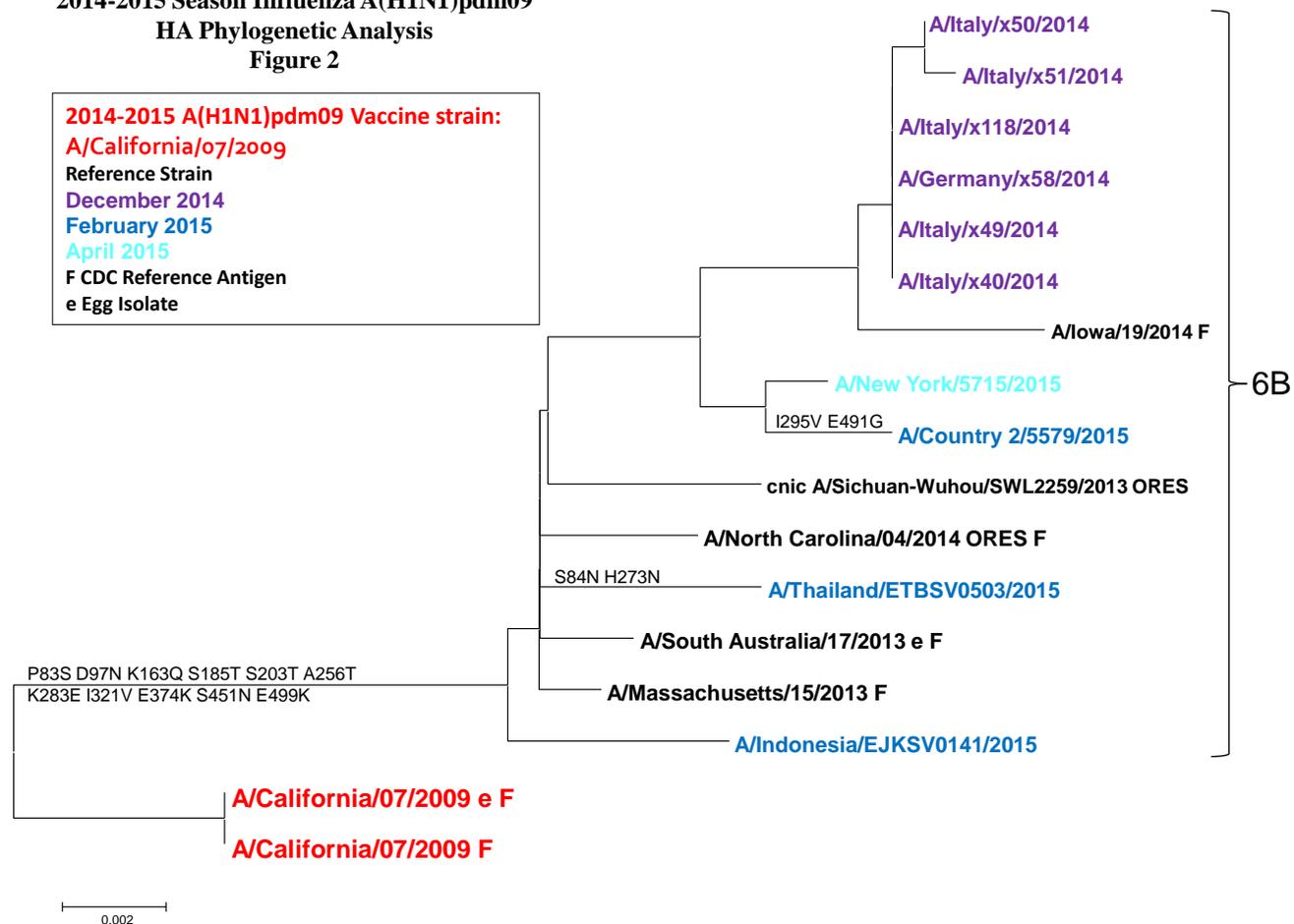


3C.3

Influenza A(H1N1)pdm09

- The sequences are characterized in a neighbor-joining phylogenetic tree with reference strains rooted from the current vaccine strain, A/California/07/2009 [Figure 2].
- The influenza A(H1N1)pdm09 specimens characterized for this report exhibited an overall protein identity of 97.5-97.8% compared to A/California/07/2009-like vaccine strain.
- All of the influenza A(H1N1)pdm09 viruses in this season contained mutations consistent with one of the circulating subgroups, referred as group 6B. Isolates of this group share two distinguishing mutations, K163Q (lysine to glutamine), and A256T (alanine to threonine).
- Of the 15 mutations present in the influenza A(H1N1)pdm09 specimens, five occurred at predicted antigenic sites and one at the receptor binding site.^{2,5}

2014-2015 Season Influenza A(H1N1)pdm09
HA Phylogenetic Analysis
Figure 2

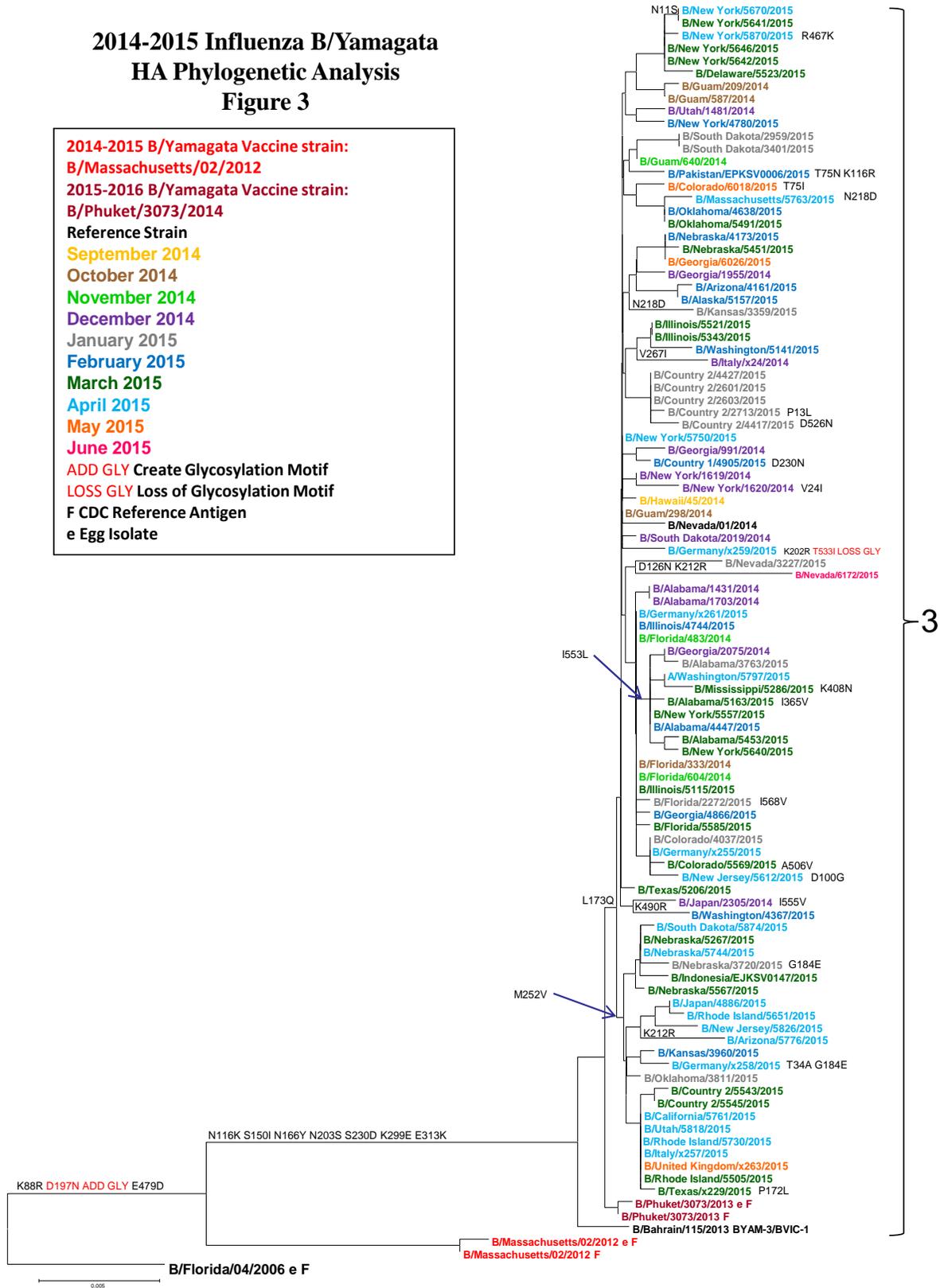


Influenza B

- The influenza B isolates are characterized in lineage specific, neighbor-joining phylogenetic trees with reference strains. The phylogenetic trees are rooted from previous vaccines, B/Florida/04/2006 for Yamagata specimens [Figure 3] and B/Ohio/01/2005 for the Victoria specimens [Figure 4].
- The distinguishing characteristic between the two lineages (Victoria & Yamagata) is defined by an amino acid deletion in viruses belonging to the Yamagata lineage.¹ Ninety-four of the influenza B specimens characterized this season resided within the Yamagata lineage (70%) while 40 resided within the Victoria lineage (30%).
- The influenza B/Yamagata specimens characterized in this report exhibited an overall protein identity of 97.2-97.7% when compared to the 2013-2014 influenza B/Yamagata vaccine strain, B/Massachusetts/02/2012-like virus. When compared to the 2013-2014 influenza B/Victoria vaccine strain, B/Brisbane/60/2008-like virus, the influenza B/Victoria specimens exhibited a protein homology of 98.6-99.6%.
- All 94 specimens of the influenza B/Yamagata lineage classify into group Y3, similar to the 2015-2016 B/Yamagata vaccine strain, B/Phuket/3073/2014-like virus.
- Thirty-nine of the Influenza B/Victoria specimens this season were characterized as being in group 1A, identified by the mutations N75K (asparagine to lysine), N165K (asparagine to lysine), and S172P (serine to proline). One specimen resided in group 1B, designated by the mutation L58P (lysine to proline) in addition to the 1A mutations.
- Observations are based solely on sequence motifs. Within the influenza B specimens characterized this season, two mutations were observed that could cause loss of a glycosylation motif: T533I (threonine to isoleucine) in the Yamagata lineage and N531D (asparagine to aspartic acid) in the Victoria lineage. Two mutations were observed that could cause a gain of glycosylation motif: D197N (aspartic acid to asparagine) in the Yamagata lineage and A199T (alanine to threonine) in the Victoria lineage.

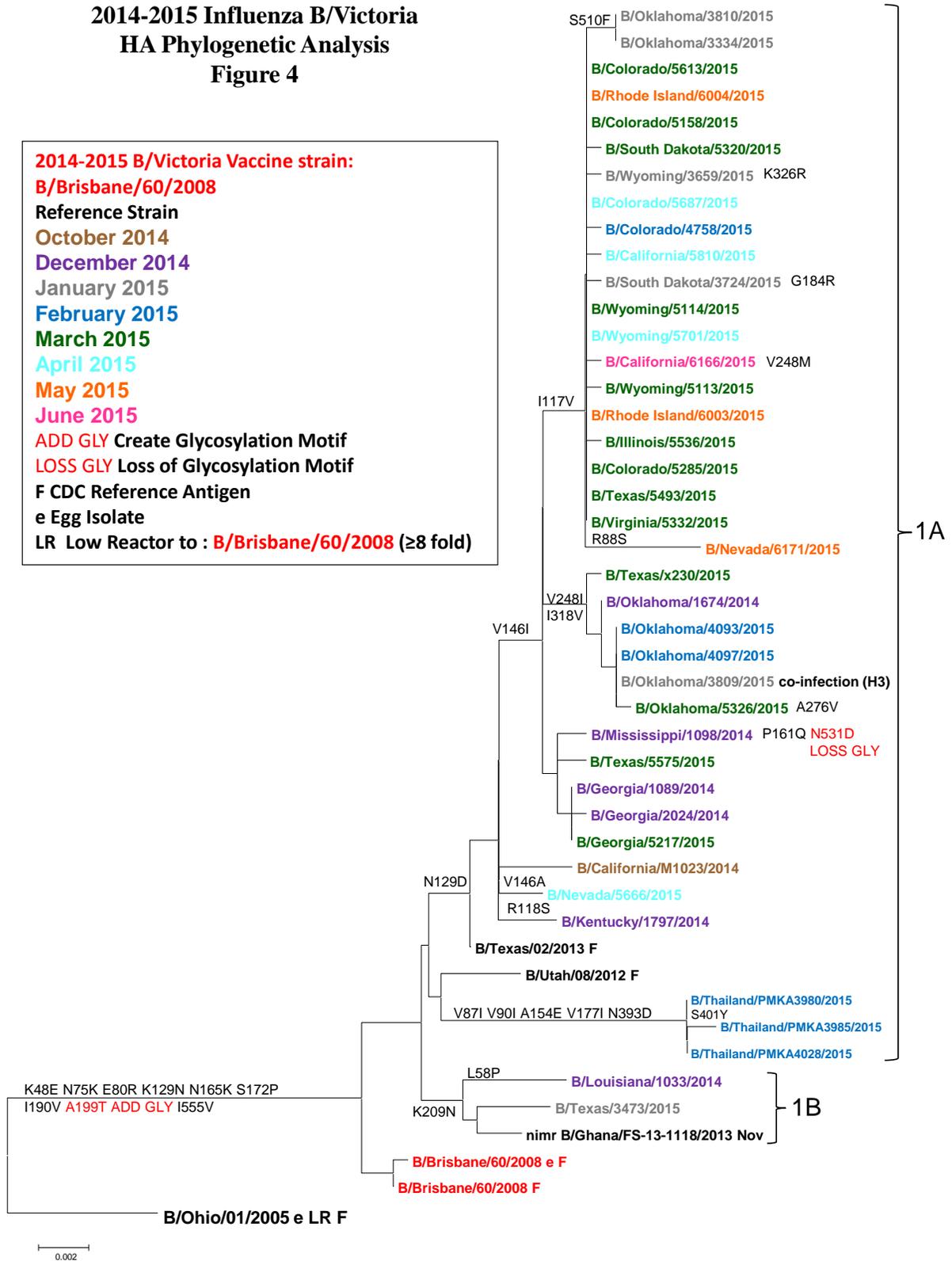
2014-2015 Influenza B/Yamagata
HA Phylogenetic Analysis
Figure 3

2014-2015 B/Yamagata Vaccine strain:
B/Massachusetts/02/2012
2015-2016 B/Yamagata Vaccine strain:
B/Phuket/3073/2014
Reference Strain
September 2014
October 2014
November 2014
December 2014
January 2015
February 2015
March 2015
April 2015
May 2015
June 2015
ADD GLY Create Glycosylation Motif
LOSS GLY Loss of Glycosylation Motif
F CDC Reference Antigen
e Egg Isolate



2014-2015 Influenza B/Victoria
HA Phylogenetic Analysis
Figure 4

2014-2015 B/Victoria Vaccine strain:
B/Brisbane/60/2008
Reference Strain
October 2014
December 2014
January 2015
February 2015
March 2015
April 2015
May 2015
June 2015
ADD GLY Create Glycosylation Motif
LOSS GLY Loss of Glycosylation Motif
F CDC Reference Antigen
e Egg Isolate
LR Low Reactor to : **B/Brisbane/60/2008** (≥ 8 fold)



References:

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2. Kongchanagul A, Suptawiwat, O, Kanrai, P, Uiprasertkul, M, Puthavathana, P, and Auewarakul P (2008) Positive selection at the receptor-binding site of haemagglutinin H5 in viral sequences derived from human tissues. *Journal of Gen. Vir.* 89, 1805-1810.
3. Cherry JL, Lipman DJ, Nikolskaya A, Wolf YI. Evolutionary Dynamics of N-Glycosylation Sites of Influenza Virus Hemagglutinin. *PLoS Curr Influenza*. 2009 August 18: RRN1001.
4. Deem, M, and Pan, K (2009). The epitope regions of H1-subtype influenza A, with application to vaccine efficacy. *Protein Engineering, Design and Selection*. 22, no. 9. 543-546.
5. Wolf YI, Viboud C, Holmes EC, Koonin EV, Lipman DJ. Long intervals of stasis punctuated by bursts of positive selection in the seasonal evolution of influenza A virus. *Biol Direct*. 2006; 1: 34. Published online 2006 October 26. doi: 10.1186/1745-6150-1-34.

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